

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/783,317A

Source: IFW0

Date Processed by STIC: 4/7/05

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RAW SEQUENCE LISTING

DATE: 04/07/2005

PATENT APPLICATION: US/10/783,317A

TIME: 08:37:16

Input Set : A:\sequence listing.TXT

Output Set: N:\CRF4\04072005\J783317A.raw

3 <110> APPLICANT: RASMUSSEN, Peter Birk
4 JENSEN, Martin Roland
5 NIELSEN, Klaus Gregorius
6 KOEFOED, Peter
7 DEGAN, Florence Dal
9 <120> TITLE OF INVENTION: Novel Method For Down-Regulation Of Amyloid
11 <130> FILE REFERENCE: 674542-2017
13 <140> CURRENT APPLICATION NUMBER: 10/783,317A
14 <141> CURRENT FILING DATE: 2004-02-20
16 <150> PRIOR APPLICATION NUMBER: PCT/DK02/00547
17 <151> PRIOR FILING DATE: 2002-08-20
19 <150> PRIOR APPLICATION NUMBER: 60/373,027
20 <151> PRIOR FILING DATE: 2002-04-16
22 <150> PRIOR APPLICATION NUMBER: PA 2002 00558
23 <151> PRIOR FILING DATE: 2002-04-16
25 <150> PRIOR APPLICATION NUMBER: 60/337,543
26 <151> PRIOR FILING DATE: 2001-10-22
28 <150> PRIOR APPLICATION NUMBER: PA 2001 01231
29 <151> PRIOR FILING DATE: 2001-08-20
31 <160> NUMBER OF SEQ ID NOS: 17
33 <170> SOFTWARE: PatentIn Ver. 3.1
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 2313
37 <212> TYPE: DNA
38 <213> ORGANISM: Homo sapiens
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42 <222> LOCATION: (1)..(2313)
44 <220> FEATURE:
45 <221> NAME/KEY: misc_feature
46 <222> LOCATION: (2098)..(2169)
47 <223> OTHER INFORMATION: nucleotides encoding transmembrane region
49 <220> FEATURE:
50 <221> NAME/KEY: misc_feature
51 <222> LOCATION: (2014)..(2313)
52 <223> OTHER INFORMATION: Nucleotides encoding C-100
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55 <221> NAME/KEY: misc_feature
56 <222> LOCATION: (2016)..(2144)
57 <223> OTHER INFORMATION: Abeta 42/43
59 <220> FEATURE:
60 <221> NAME/KEY: misc_feature
61 <222> LOCATION: (2014)..(2142)

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62 <223> OTHER INFORMATION: Abeta 42/43

64 <400> SEQUENCE: 1

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69 gcg ctg gag gta ccc act gat ggt aat gct ggc ctg ctg gct gaa ccc      96
70 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
71           20           25           30
73 cag att gcc atg ttc tgt ggc aga ctg aac atg cac atg aat gtc cag      144
74 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
75           35           40           45
77 aat ggg aag tgg gat tca gat cca tca ggg acc aaa acc tgc att gat      192
78 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
79           50           55           60
81 acc aag gaa ggc atc ctg cag tat tgc caa gaa gtc tac cct gaa ctg      240
82 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
83   65           70           75           80
85 cag atc acc aat gtg gta gaa gcc aac caa cca gtg acc atc cag aac      288
86 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
87           85           90           95
89 tgg tgc aag cgg ggc cgc aag cag tgc aag acc cat ccc cac ttt gtg      336
90 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
91           100          105          110
93 att ccc tac cgc tgc tta gtt ggt gag ttt gta agt gat gcc ctt ctc      384
94 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
95           115          120          125
97 gtt cct gac aag tgc aaa ttc tta cac cag gag agg atg gat gtt tgc      432
98 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
99           130          135          140
101 gaa act cat ctt cac tgg cac acc gtc gcc aaa gag aca tgc agt gag      480
102 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
103 145           150          155          160
105 aag agt acc aac ttg cat gac tac ggc atg ttg ctg ccc tgc gga att      528
106 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
107           165          170          175
109 gac aag ttc cga ggg gta gag ttt gtg tgt tgc cca ctg gct gaa gaa      576
110 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
111           180          185          190
113 agt gac aat gtg gat tct gct gat gcg gag gag gat gac tcg gat gtc      624
114 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
115           195          200          205
117 tgg tgg ggc gga gca gac aca gac tat gca gat ggg agt gaa gac aaa      672
118 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
119           210          215          220
121 gta gta gaa gta gca gag gag gaa gaa gtg gct gag gtg gaa gaa gaa      720
122 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
123 225           230          235          240
125 gaa gcc gat gat gac gag gac gat gag gat ggt gat gag gta gag gaa      768
126 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu

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127		245		250		255		
129	gag gct gag gaa ccc tac gaa gaa gcc aca gag aga acc acc agc att							816
130	Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile							
131		260		265		270		
133	gcc acc acc acc acc acc acc aca gag tct gtg gaa gag gtg gtt cga							864
134	Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg							
135		275		280		285		
137	gag gtg tgc tct gaa caa gcc gag acg ggg ccg tgc cga gca atg atc							912
138	Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile							
139		290		295		300		
141	tcc cgc tgg tac ttt gat gtg act gaa ggg aag tgt gcc cca ttc ttt							960
142	Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe							
143	305		310		315		320	
145	tac ggc gga tgt ggc ggc aac cgg aac aac ttt gac aca gaa gag tac							1008
146	Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr							
147		325		330		335		
149	tgc atg gcc gtg tgt ggc agc gcc atg tcc caa agt tta ctc aag act							1056
150	Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr							
151		340		345		350		
153	acc cag gaa cct ctt gcc cga gat cct gtt aaa ctt cct aca aca gca							1104
154	Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala							
155		355		360		365		
157	gcc agt acc cct gat gcc gtt gac aag tat ctc gag aca cct ggg gat							1152
158	Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp							
159		370		375		380		
161	gag aat gaa cat gcc cat ttc cag aaa gcc aaa gag agg ctt gag gcc							1200
162	Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala							
163	385		390		395		400	
165	aag cac cga gag aga atg tcc cag gtc atg aga gaa tgg gaa gag gca							1248
166	Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala							
167		405		410		415		
169	gaa cgt caa gca aag aac ttg cct aaa gct gat aag aag gca gtt atc							1296
170	Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile							
171		420		425		430		
173	cag cat ttc cag gag aaa gtg gaa tct ttg gaa cag gaa gca gcc aac							1344
174	Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn							
175		435		440		445		
177	gag aga cag cag ctg gtg gag aca cac atg gcc aga gtg gaa gcc atg							1392
178	Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met							
179		450		455		460		
181	ctc aat gac cgc cgc cgc ctg gcc ctg gag aac tac atc acc gct ctg							1440
182	Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu							
183	465		470		475		480	
185	cag gct gtt cct cct cgg cct cgt cac gtg ttc aat atg cta aag aag							1488
186	Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys							
187		485		490		495		
189	tat gtc cgc gca gaa cag aag gac aga cag cac acc cta aag cat ttc							1536
190	Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe							
191		500		505		510		

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194 Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
195      515      520      525
197 cag gtt atg aca cac ctc cgt gtg att tat gag cgc atg aat cag tct 1632
198 Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
199      530      535      540
201 ctc tcc ctg ctc tac aac gtg cct gca gtg gcc gag gag att cag gat 1680
202 Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
203 545      550      555      560
205 gaa gtt gat gag ctg ctt cag aaa gag caa aac tat tca gat gac gtc 1728
206 Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
207      565      570      575
209 ttg gcc aac atg att agt gaa cca agg atc agt tac gga aac gat gct 1776
210 Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
211      580      585      590
213 ctc atg cca tct ttg acc gaa acg aaa acc acc gtg gag ctc ctt ccc 1824
214 Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
215      595      600      605
217 gtg aat gga gag ttc agc ctg gac gat ctc cag ccg tgg cat tct ttt 1872
218 Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
219      610      615      620
221 ggg gct gac tct gtg cca gcc aac aca gaa aac gaa gtt gag cct gtt 1920
222 Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
223 625      630      635      640
225 gat gcc cgc cct gct gcc gac cga gga ctg acc act cga cca ggt tct 1968
226 Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
227      645      650      655
229 ggg ttg aca aat atc aag acg gag gag atc tct gaa gtg aag atg gat 2016
230 Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
231      660      665      670
233 gca gaa ttc cga cat gac tca gga tat gaa gtt cat cat caa aaa ttg 2064
234 Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
235      675      680      685
237 gtg ttc ttt gca gaa gat gtg ggt tca aac aaa ggt gca atc att gga 2112
238 Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
239      690      695      700
241 ctc atg gtg ggc ggt gtt gtc ata gcg aca gtg atc gtc atc acc ttg 2160
242 Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
243 705      710      715      720
245 gtg atg ctg aag aag aaa cag tac aca tcc att cat cat ggt gtg gtg 2208
246 Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
247      725      730      735
249 gag gtt gac gcc gct gtc acc cca gag gag cgc cac ctg tcc aag atg 2256
250 Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
251      740      745      750
253 cag cag aac ggc tac gaa aat cca acc tac aag ttc ttt gag cag atg 2304
254 Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
255      755      760      765
257 cag aac tag 2313

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263 <211> LENGTH: 770
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapiens
267 <400> SEQUENCE: 2
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272      20          25          30
274 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
275      35          40          45
277 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
278      50          55          60
280 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
281      65          70          75          80
283 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
284      85          90          95
286 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
287      100         105         110
289 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
290      115         120         125
292 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
293      130         135         140
295 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
296      145         150         155         160
298 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
299      165         170         175
301 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
302      180         185         190
304 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
305      195         200         205
307 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
308      210         215         220
310 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
311      225         230         235         240
313 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
314      245         250         255
316 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
317      260         265         270
319 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
320      275         280         285
322 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
323      290         295         300
325 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
326      305         310         315         320
328 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
329      325         330         335

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VERIFICATION SUMMARY

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